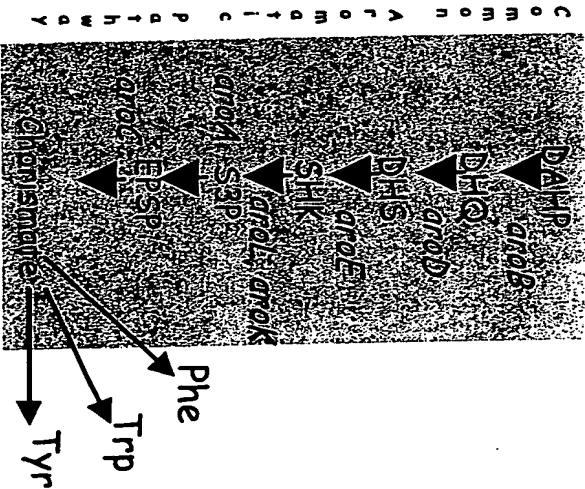


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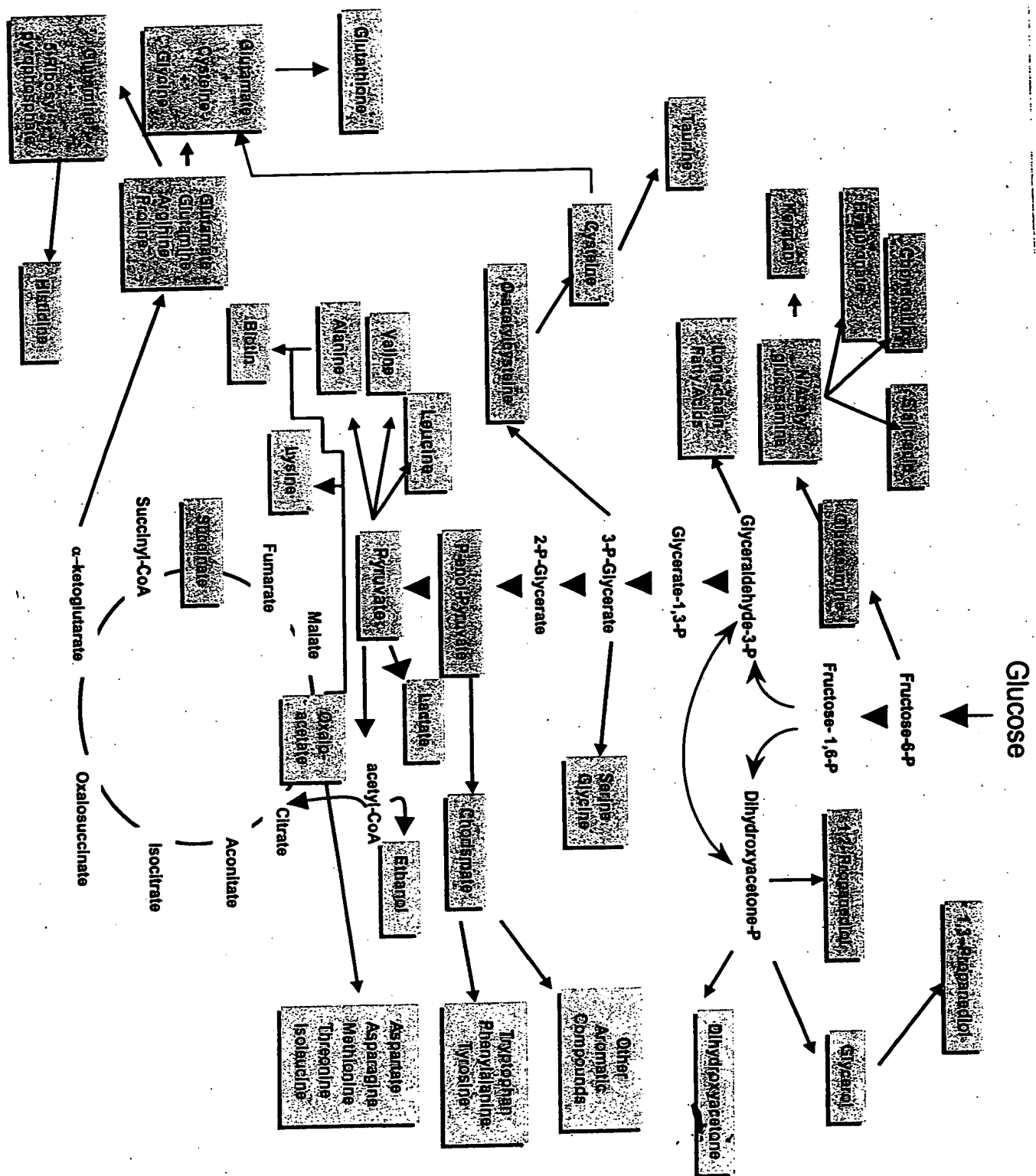


FIG. 2

TCGGTTTTTCACAGTTGTTACATTTCTTTTCAGTAAAGTCTGGATGCATATGGC
GGCCGCATAACTTCGTATAGCATACATTATACGAAGTTATCTAGAGTTGCATGC
CTGCAGGTCCGAATTTCTGCCATTTCATCCGCTTATTATCACTTATTCAGGCGT
AGCACCAGGCGTTTAAGGGCACCAATAACTGCCTTAAAAAAATTACGCCCC
GCCCTGCCACTCATCGCAGTACTGTTGTAATTCATTAAGCATTCTGCCGA
CATGGAAGCCATCACAAACGGCATGATGAACCTGAATCGCCAGCGGCAT
CAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAAACGGGG
GCGAAGAAGTTGTCCATATTGGCCACGTTTAAATCAAACTGGTGAAAC
TCACCCAGGGATTGGCTGAGACGAAAAACATATTCTCAATAAACCCTTTA
GGGAAATAGGCCAGGTTTTACCGTAACACGCCACATCTTGCGAATATA
TGTGTAGAACTGCCGGAAATCGTCGTGGTATTCACTCCAGAGCGATGA
AAACGTTTCAGTTTGCTCATGGAAAACGGTGTAACAAGGGTGAACTA
TCCCATATCACCAGCTCACCGTCTTTCATTGCCATACGGAATTCCGGATG
AGCATTATCAGGCGGGCAAGAATGTGAATAAAGGCCGGATAAACTTG
TGCTTATTTTTCTTTACGGTCTTTAAAAAGGCCGTAATATCCAGCTGAAC
GGTCTGGTTATAGGTACATTGAGCAACTGACTGAAATGCCTCAAAATGTT
CTTTACGATGCCATTGGGATATATCAACGGTGGTATATCCAGTGATTTT
TTCTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGATAACTCAAAAATAC
GCCCGGTAGTGATCTTATTTCAATTATGGTGAAAGTTGGAACCTCTTACGTGCC
GATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACA
GGGACACCAGGATTTATTTATTCTGCGAAGTGATCTTCCGTCACAGGTATTTA
TTCGGACTCTAGATAACTTCGTATAGCATACATTATACGAAGTTATGGATCATG
GCTGTGCAGGTGCTAAATCACTGCATAATTCGTGTGCTCAAGGCGCACTCCC
GTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTTCTGGCAAATATTCT
GAAATGAGCTGTTGACAATTAATCATCCGGCTCGTATAATGTGTGGAATTGTG
AGCGGATAACAATTTACACACAGGAAACAGACTAATTCACAATAAAAAATAACC
ATATTGGAGGGGCATCATG

FIG. 3

CAGCAGTGGTGGTGATCGGTTTTGGCTGGGGCCCCTCCCCGCACCGGAG
GCCGATTACAGCCAACCACAACAGGCAAAGGGTTTGGAAGATATTCATA
TTATTATTGCGGTTGTCACAGTTGTTACATTTCTTTTCAGTAAAGTCTGG
ATGCATATGGCGGCCCGCATAACTTCGTATAGCATAACATTATACGAAGTTATGGATC
ATGGCTGTGCAGGTCGTAAATCACTGCATAATTGGTGTGCTCAAGGCGCACT
CCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTTCTGGCAAATATT
CTGAAATGAGCTGTTGACAATTAATCATCCGGCTCGTATAATGTGTGGCATTG

FIG. 4

ACTTAGTTTGCCCAGCTTGCAAAAAGGCATCGCTGCAATTGGATGCATATGG
CGGCCGCATAACTTCGTATAGCATACATTATACGAAGTTATCTAGAGTTGCATG
CCTGCAGGTCCGAATTTCTGCCATTCATCCGCTTATTATCACTTATTCAGGCGT
AGCACCAGGCGTTTAAGGGCACCAATAACTGCCTTAAAAAAATTACGCCCC
GCCCTGCCACTCATCGCAGTACTGTTGTAATTCATTAAGCATTCTGCCGA
CATGGAAGCCATCACAAACGGCATGATGAACCTGAATCGCCAGCGGCAT
CAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAAACGGGG
GCGAAGAAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAAC
TCACCCAGGGATTGGCTGAGACGAAAAACATATTCTCAATAAACCTTTA
GGGAAATAGGCCAGGTTTTACCCGTAACACGCCACATCTTGCGAATATA
TGTGTAGAAACTGCCGGAAATCGTCGTGGTATTCACTCCAGAGCGATGA
AAACGTTTCAGTTTGCTCATGGAAAAACGGTGTAACAAGGGTGAACACTA
TCCCATATCACCAGCTCACCGTCTTTTCATTGCCATACGGAATTCCGGATG
AGCATTTCATCAGGCGGGCAAGAATGTGAATAAAGGCCGGATAAACTTG
TGCTTATTTTTCTTTACGGTCTTTAAAAAGGCCGTAATATCCAGCTGAAC
GGTCTGGTTATAGGTACATTGAGCAACTGACTGAAATGCCTCAAAATGTT
CTTTACGATGCCATTGGGATATATCAACGGTGGTATATCCAGTGATTTTT
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GCCCGGTAGTGATCTTATTTTCATTATGGTGAAAGTTGGAACCTCTTACGTGCC
GATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACA
GGGACACCAGGATTTATTTATTCTGCGAAGTGATCTTCCGTACAGGTATTTA
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GCTGTGCAGGTCGTAAATCACTGCATAATTTCGTGTCGCTCAAGGCGCACTCCC
GTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTTCTGGCAAATATTCT
GAAATGAGCTGCTGACAATTAATCATCCGGCTCGTATAATGTGTGGAATTGTG
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AGCGGAGCAGTTGAAGAATG

FIG. 5

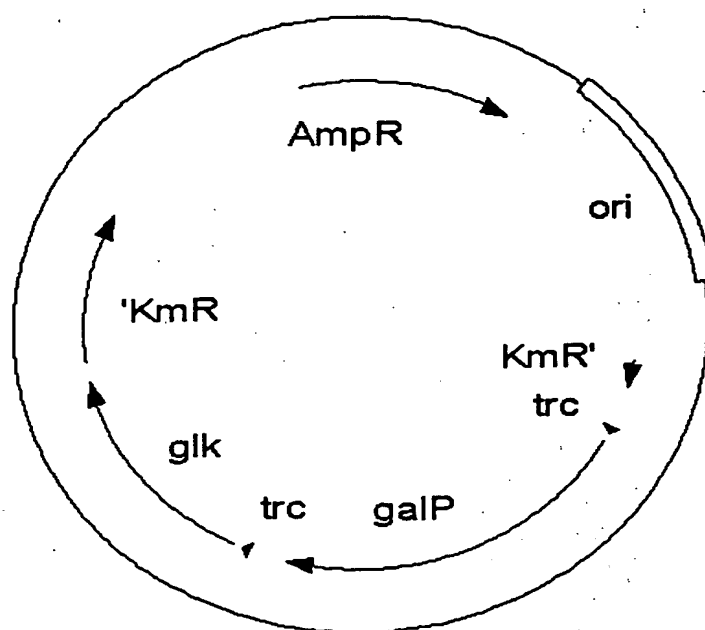


FIG. 6

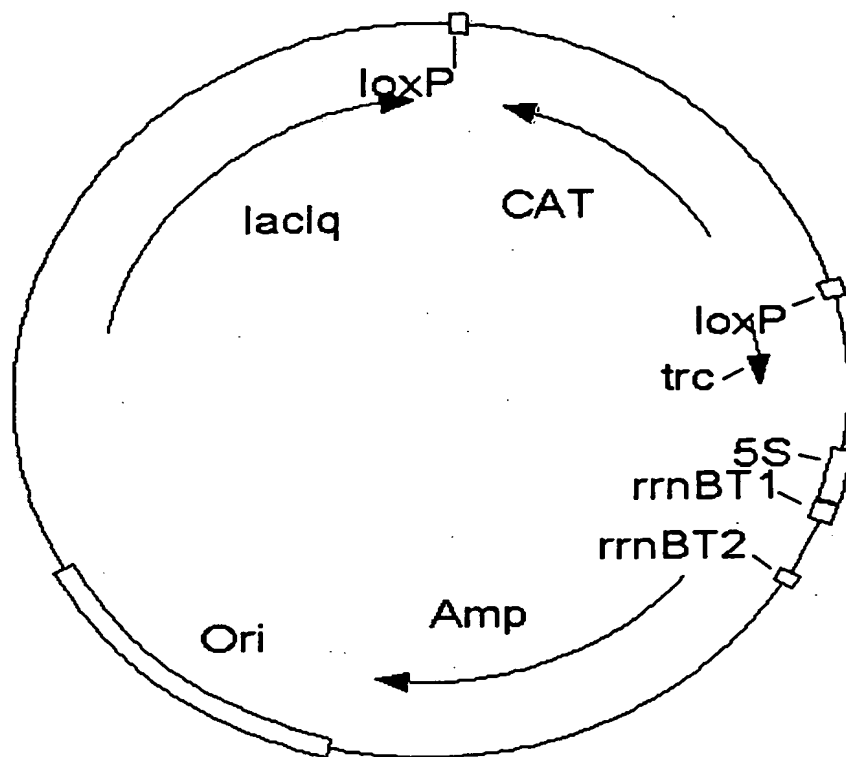


FIG. 7A.

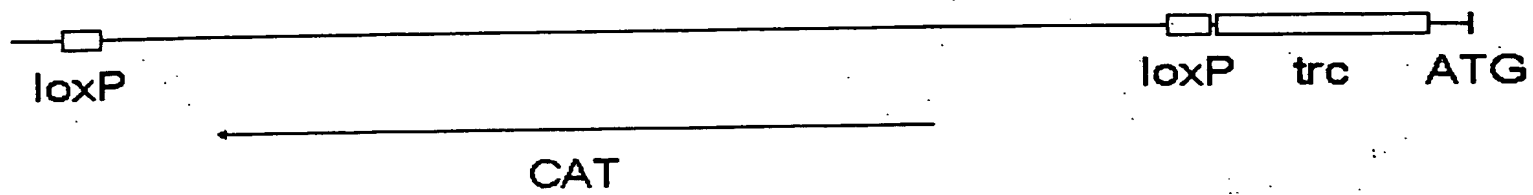


FIG. 7B

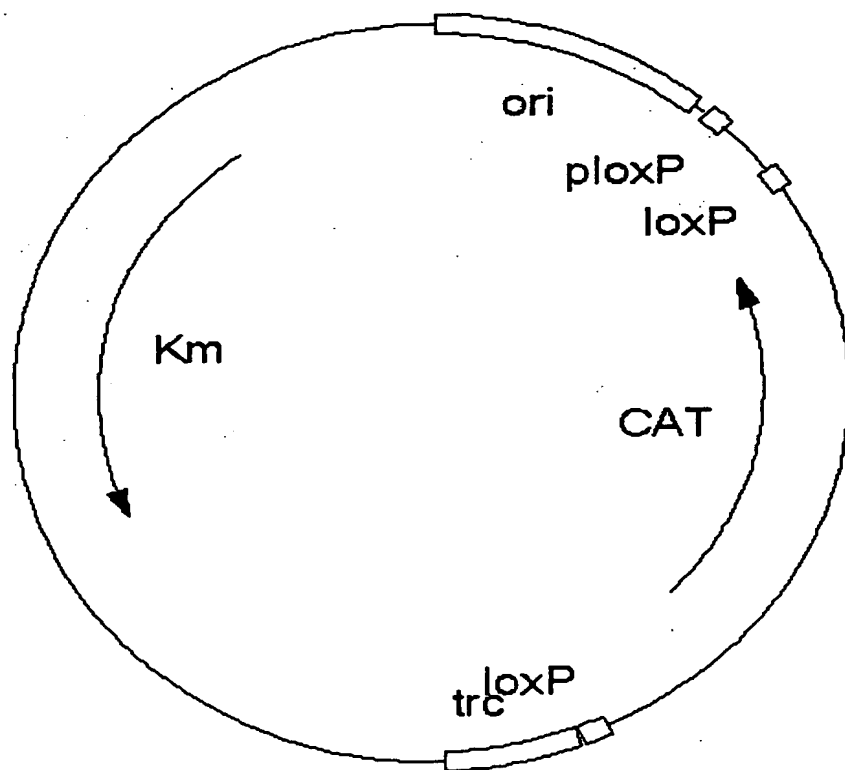


FIG. 8.

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ATGTTCTCTTGCTTTTGTGAGCAAGATAGCCAGATCAATGTCGATCGTGGCTGGCTC
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ACCGACTCTTTGGATGGCAGCAGAAGCGTTGTTACCCAGCCTAGACCTTCGACGA
AACCACAACCTAAGGCAACAACGTTCTTCAAAGCACCACAGATGGAGATACCAGCA
ACATCTTCGATGACACTAACGTGGAAGTAAGGTCTGTGGAACAAGGCCTTTAGAAC
CTTATGGTCGACGTCCTTGCCCTCGCCTCTGAAATCCTTTGGAATGTGGTAAGCAA
CTGTTGTTTCAGACCAGTGTTCTTGAGCGACTTCGGTGGCAATGTTAGCACCAGAT
AGAGCACCACATTGAATACCTAGTTCCTCAGTGATGTAAGAGGATAGCAATTGGAC
ACCTTTAGCACCAACTTCAAACCCCTTTAGACAGGAGATAGCTCTGACGTGTGAATC
AACATGACCTTTCAATTGGCTACAGATACGGGGCAAAAATTGATGTGGAATGTTGAA
AACGATGATGTCGACATCCTTGACTGAATCAATCAAGTCTGGATTAGCAACCAAATT
GTCGGGTAGAGTGATGCCAGGCAAGTATTTACGTTTTGATGTCTAGTATTTATGAT
TTCAGTCAATTTTTACCATTTGATCTCTTCTTCGAACACCCACATTTGTACTATTGGA
GCGAAAACCTTCTGGGTATCCCTTACAATTTTCGGCAACCACCTTGGCAATAGTAGTA

CCCCAGTTACCAGATCCAATCACAGTAACCTTGAAAGGCTTTTCGGCAGCCTTCAA
AGAAACAGAAGAGGAAGTTCTCTTTCTACCAGCATTCAAGTGGCCGGAAGTTAAGT
TTAATCTATCAGCAGCAGCAGCCATGGAATTGTCCTCCTTACTAGTCATGGTCTGTT
TCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACATTATACGAGCCGGATGATT
AATTGTCAACAGCTCATTTCAGAATATTTGCCAGAACC GTTATGATGTCGGCGCAAA
AAACATTATCCAGAACGGGAGTGCGCCTTGAGCGACACGAATTATGCAGTGATTTA
CGACCTGCACAGCCATACCACAGCTTCCGATGGCTGCCTGACGCCAGAAGCATTG
GTGCACGCTAGCCAGTACATTTAAATGGTACCCTCTAGTCAAGGCCTTAAGTGAGT
CGTATTACGGACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTT
ACCCA ACTTAATCGCCTTG CAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGA
AGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGG
CGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCCGCATATG
GTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACC
CGCCAACACCCGCTGACGAGCT

FIG. 9

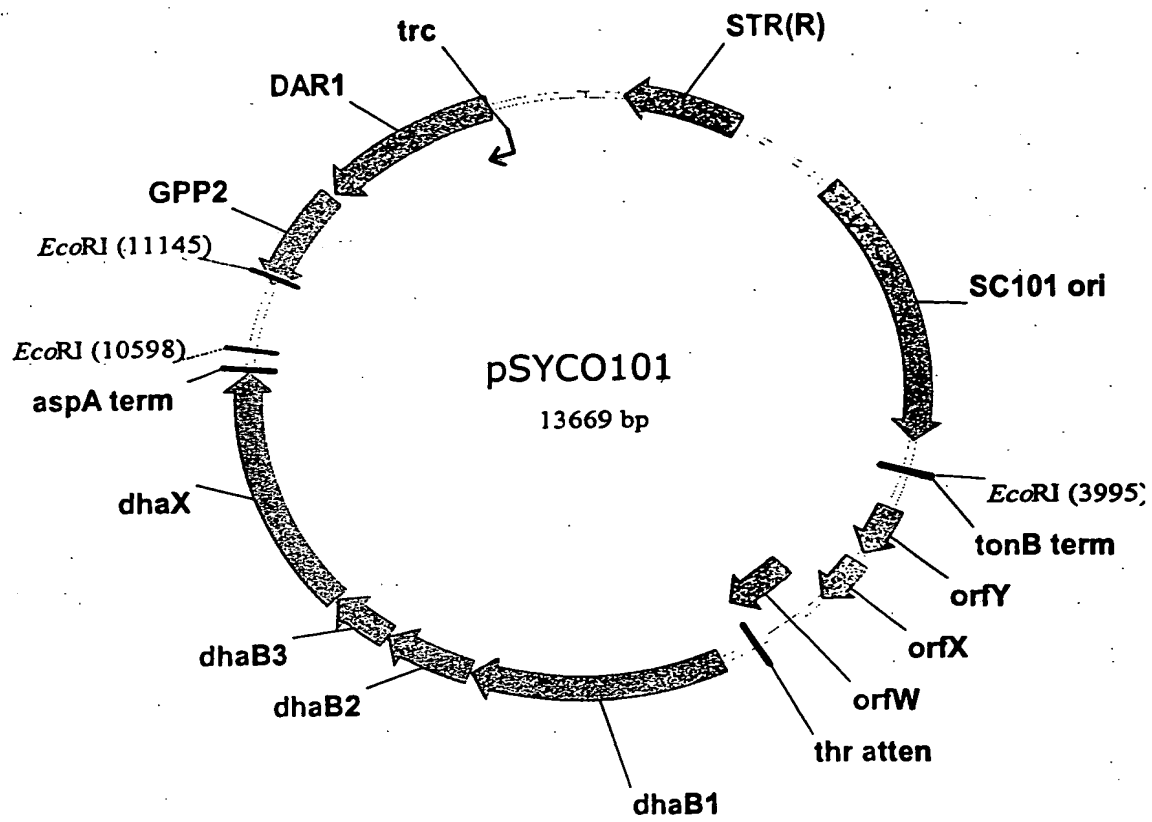
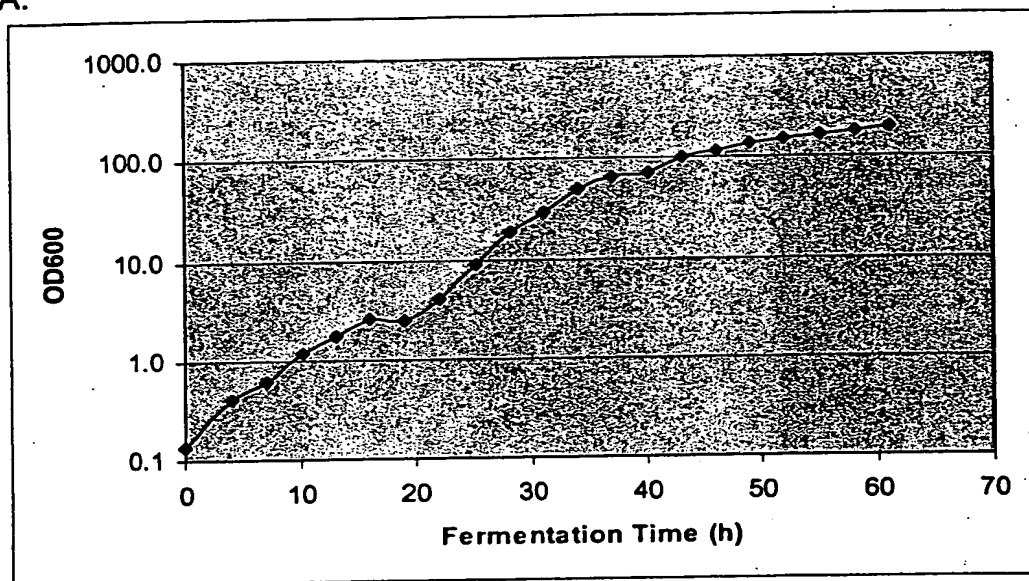


FIG. 10.

A.



B.

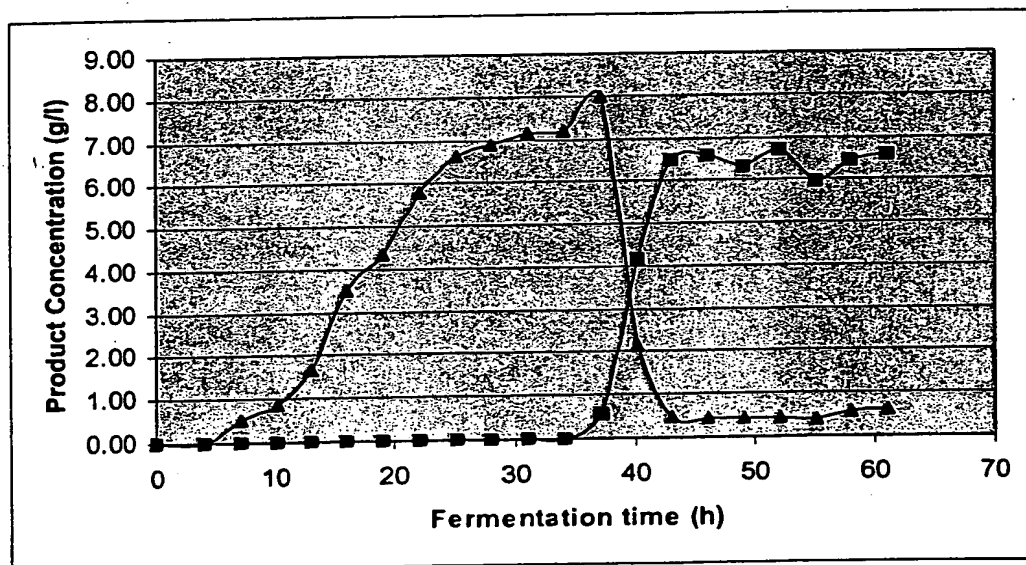
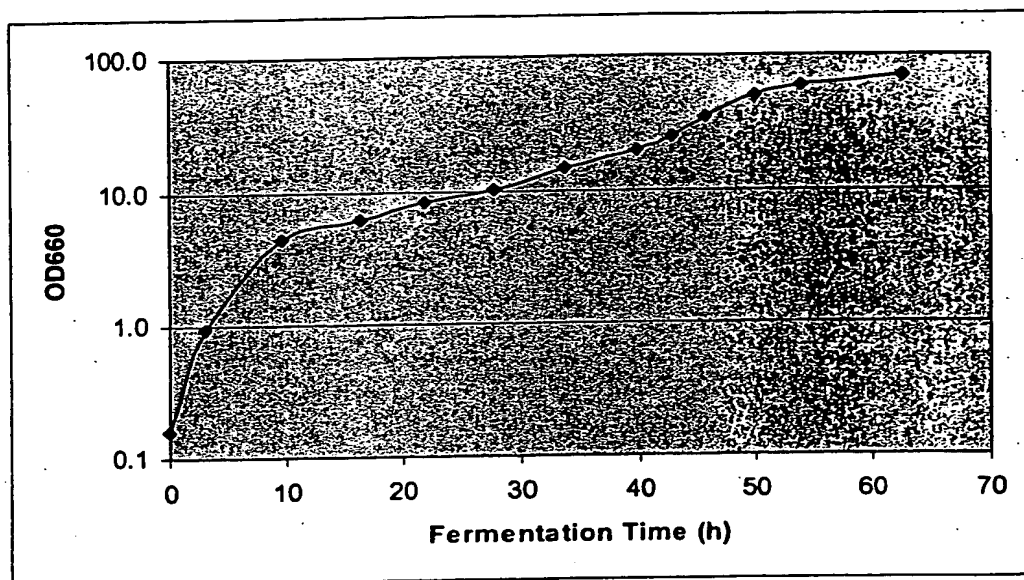


FIG. 11

A.



B.

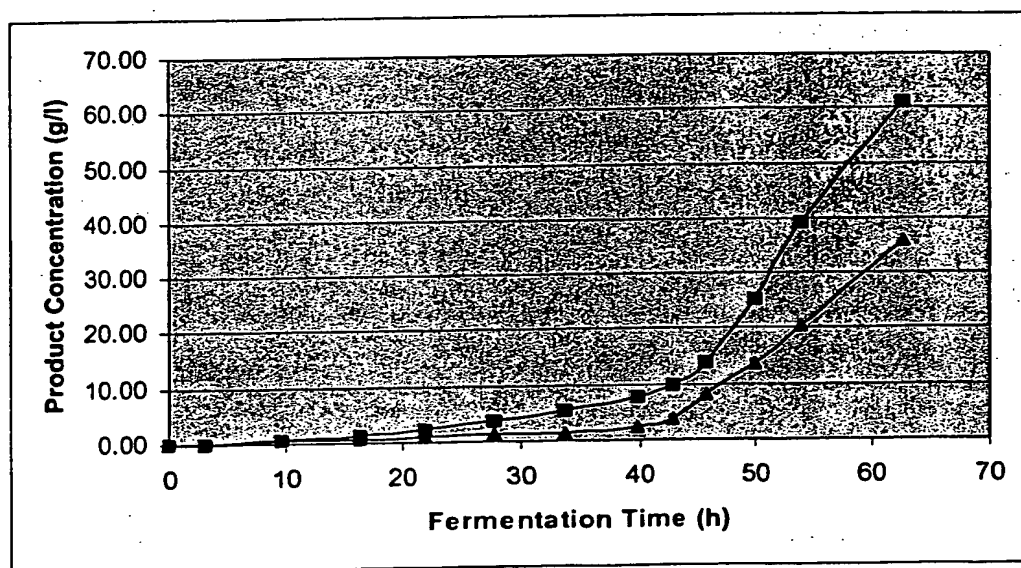
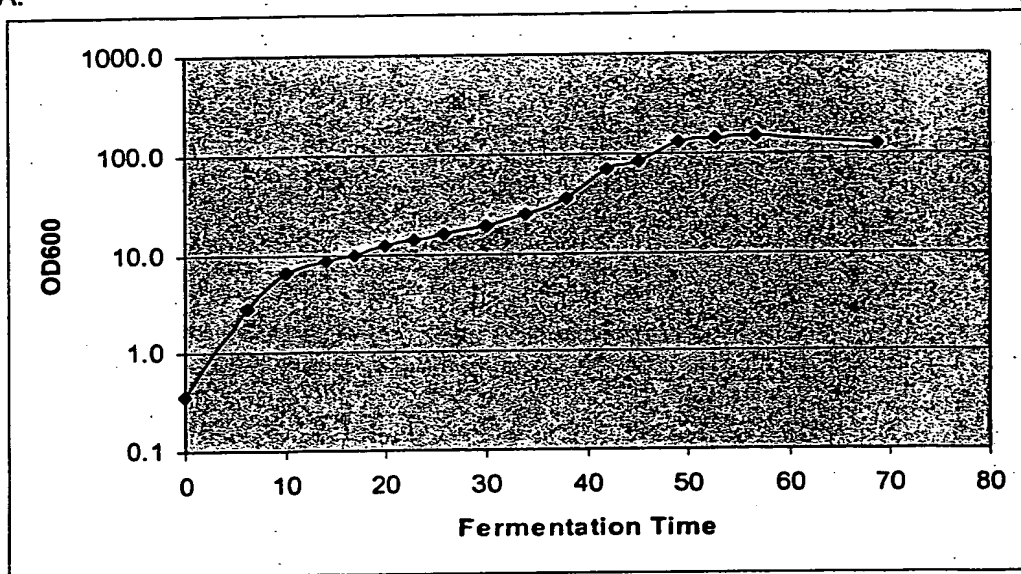
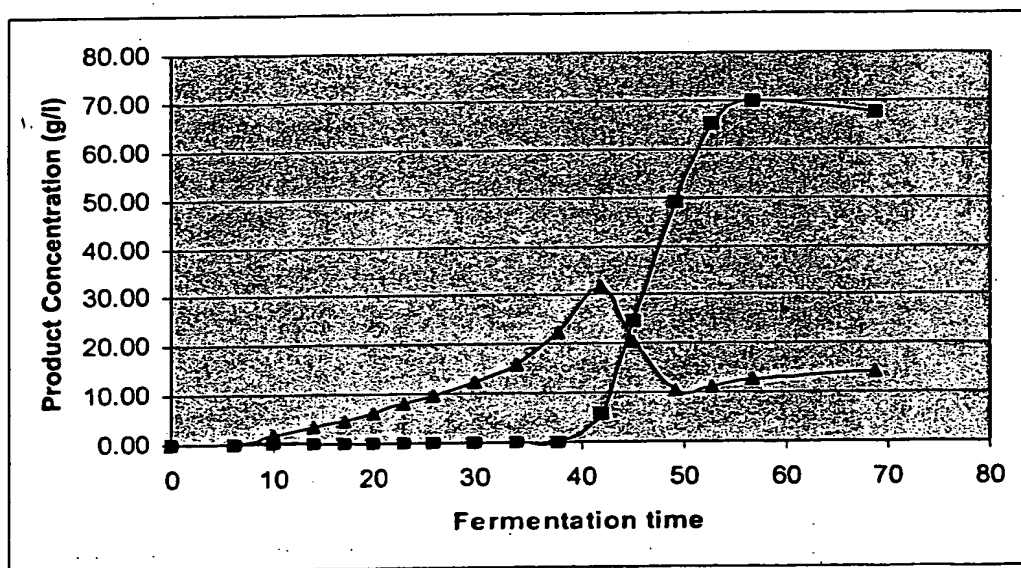


FIG. 12

A.



B.



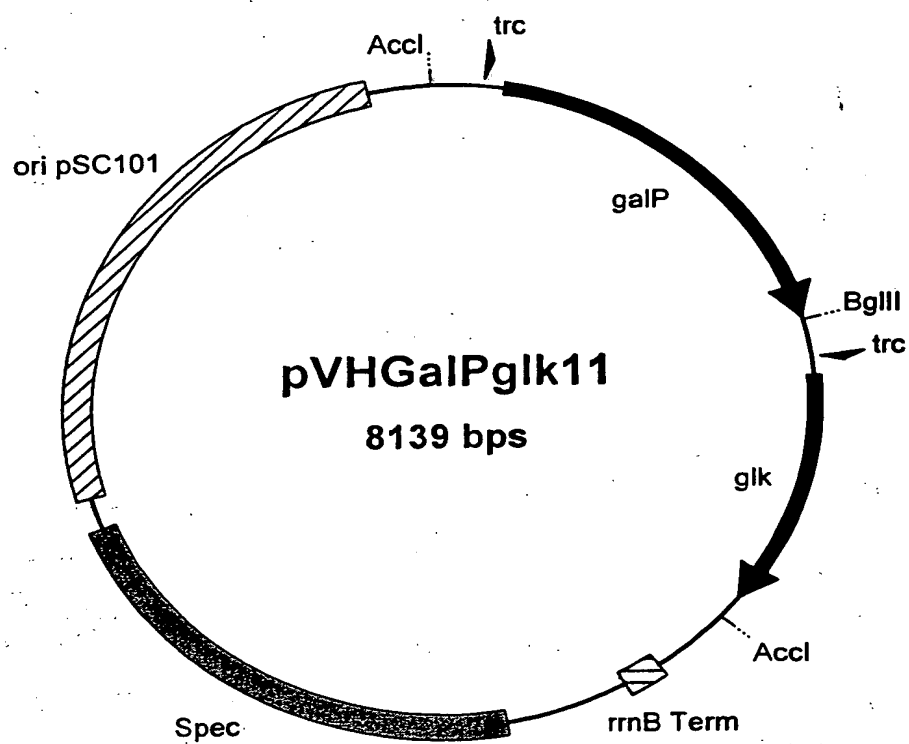


FIG. 13

ATAATTGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTGGCCGACATCAACGGTTCTGGCAAATATTCTGAAATGAGCTGTTGACAA 200
TATTAGCACAGCGAGTTCGCGTGAGGGCAAGACCTATTACAAAAACGGCGCTGTAGTATTGCCAAGACCGTTTATAAGACTTTTACTCGACAACCTGTT

Trc Pro -

TTAATCATCCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAAATTCACACAGGAACAGACCATGCCTGACGCTAAAAACAGGGCGGTCAAAAC 300
AATTAGTAGCGCGACATATTACACACCTTAACACCTCGCCTATTGTTAAAGTGTCCTTTGTCTGGTACGGACTGCGATTTTTTGTCCCGCCAGTTTG

Trc Promoter

Met Pro Asp Ala Lys Lys Gln Gly Arg Ser Asn
galP

AAGGCAATGACGTTTTTCGTCTGCTTCCTTGCCGCTCTGGCGGATTACTCTTTGGCCTGGATATCGGTGTAATTGCTGGCGCACTGCCGTTTATTGCAG 400
TTCCGTTACTGCAAAAAGCAGACGGAAGAACGGCGAGACCGCCCTAATGAGAAACCGGACCTATAGCCACATTAAACGACCGCTGACGGCAATAACGTC

Lys Ala Met Thr Phe Phe Val Cys Phe Leu Ala Ala Leu Ala Gly Leu Leu Phe Gly Leu Asp Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala
galP

ATGAATTCAGATTACTTCGCACACGCAAGAATGGTCTGAAGCTCCATGATGTTTCGGTGGCGAGTCGGTGGCGAGCGGCTGCTCTCTTTAA 500
TACTTAAGGTCTAATGAAGCGTGTGCTTCTTACCCAGCATTCGAGGTACTACAAGCCACCGCTCAGCCACCGCTCGCCGACCGAGAGGAAAT

Asp Glu Phe Gln Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys
galP

ACTCGGGCGCAAAAGAGCCCTGATGATCGGGCAATTTTGTGTCGGGTTCGCTGTTCTCTCGGGCTGCGCCAAACGTTGAAGTACTGATTCCTTCC 600
TGAGCCCGCGTTTTTCTCGGACTACTAGCCGCGTTAAACAACAACGCGCAAGGACACAAGAGACGCGCGGTTTGCAACTTCATGACTAAGAAAGG

Leu Gly Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser Leu Phe Ser Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser
galP

CGCGTTCTACTGGGGTGGCGGTGGGTGTCCTTATACCGCACCGCTGTACCTCTCTGAAATTGGCGCGGAAAAAATTCGTGGCAGTATGATCTCGA 700
GCGCAAGATGACCCCGACCGCCACCCACCGGAGAAATATGGCGTGGCGACATGGAGAGACTTTAACGCGGCCCTTTTTTAAGCACCGTCTACTAGAGCT

Arg Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
galP

FIG. 14A

CGTCGGCGCAGTATTTCGCCATCGCCATGCTGCTGATGTTTATTGTCGGTTTTGCCATGAGTGCCGTCGGCTGATTTGGGTACTGTGCTCCGAAATTCA 1400
GCAGCCGGCTCATAAAGCGGTACGACGACTACAAA TAACAGCCAAAACGGTACTCAGGCCAGGCGACTAAACCCATGACACGAGGCTTTAAGT
Pro Ser Ala Gln Tyr Phe Ala Ile Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro Leu Ile Trp Val Leu Cys Ser Glu Ile Gln
—galP—

FIG. 14B

CCGCGACTTTCGGCGCTAAACCGTAGTGGACGAGGTGCTGACCTAACGGTTGTACTAGCAACCGGTTGCAAGGACTGGTACGAGTTGTGTC
 Pro Leu Lys Gly Arg Asp Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr
 _____galp_____

CTGGGTAACGCCAACACCTTCTGGGTGTATCGGCTCTGAACGTACTGTTTATCCTGCTGACATTGTGGCTGGTACCGGAAACCAACACAGTTTCGCTGG 1600
 GACCCATTGCGGTTGTGGAGACCCACATACGCCGAGACTTGCAATGACAAATAGGACGACTGTAAACACCGACCATGGCCTTTGGTTTGTGCAAGCGGACC
 Leu Gly Asn Ala Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr Trp Leu Val Pro Glu Thr Lys His Val Ser Leu
 _____galp_____

AACATATTGAACGTAATCIGATGAAAGGTGCTAAACTCGCGGAAATAGGCGCTCACGATTAACTCCCCAAGCTTCCCTCCCATGCGGAGGAAACCCACCT 1700
 TTGTATAACTTGCATTAGACTACTTTCAGCAATTTGACGCGCTTATCCGCGAGTGCTAAATTAGAGGGGTTCGAAGGAGGGTAGCGCTCCTTTGGTGGA
 Glu His Ile Glu Arg Asn Leu Met Lys Gly Arg Lys Leu Arg Glu Ile Gly Ala His Asp
 _____galp_____

CTTCGAGTCACTTTTCTTCGCTCTATCCTTCGCGCTAATCCATATGACTAGATCTGCAGAAATTCGCCCTTAAGGAAGCTGTGGTATGGCTGTGCAGGT 1800
 GAACGTCAGTAGAAAAGAAGCGGAGATAGGAGCGGCGATTAGGTATACTGATCTAGACGCTCTTAAGCGGGAAATTCCTTCGACACCATACCGACACGTCCTCA
 CGTAAATCACTGCATAATTGCTGTGGCTCAAGGGCGCACICCCGTTCTGGATAATGTTTTTGC CGCGACATCATACGTTCTGGCAAATATTCTGAAAT 1900
 GCATTTAGTGACGTATTAAAGCACAGCGAGTTCGCGGTGAGGGCAAGACCTATTACAAAAACGGGCTGTAGTATTGCCAAGACCGTTTATAAGACTTTA
 GAGCTGTTGACAAATTAATCATCCGGCTCGTATAATGTGIGGAAATTGAGCGGATAACAAATTCACACAGGAAACAGACCATGACAAAGTATGCATTAGT 2000
 CTCGACAACTGTTAATTAGTAGCGCGAGCATATTACACACCTTAACACTCGCCTATTGTTAAAGTGTGCTCCTTTGCTGGTACTGTTTCATACGTAATCA
 Met Thr Lys Tyr Ala Leu Val
 _____glk_____

CCGTGATGTGGGCGCACCAACGCACGCTTGTGCTGTGTGATATTGCCAGTGGTGAAATCTCGCAGGCTAAGACCTATTACAGGCTTGATTACCCCCAGC 2100
 GCCACTACACCCCGCGTGGTGGTGCAGAACGAGACACACTATAACGGTCACCACCTTAGAGCGTCCGATTCTGGATAAGTCCCGAACTAATGGGGTGG
 Gly Asp Val Gly Thr Asn Ala Arg Leu Ala Leu Cys Asp Ile Ala Ser Gly Glu Ile Ser Gln Ala Lys Thr Tyr Ser Gly Leu Asp Tyr Pro Ser
 _____glk_____

CTCGAAGCGGTCATTCCGCTTATCTTGAAGAACATAAGGTGAGGTGAAAGACGGCTGTATTGCCATCGCTTGCCCAATTACCGGTGACTGGGTGGCGA 2200
 GAGCTTCGCCAGTAAGCGCAATAGAACTTCTTGATTCCAGCTCCACTTCTGCCGACATAACGGTAGCGAAGGGTTAATGGCCACTGACCCACCCGCT
 Leu Glu Ala Val Ile Arg Val Tyr Leu Glu Glu His Lys Val Glu Val Lys Asp Gly Cys Ile Ala Ile Ala Cys Pro Ile Thr Gly Asp Trp Val Ala
 _____glk_____



FIG. 14C

ACTGGTTGGTATGGACCCGCAAGAGTTAACGGCTTTACTTTTTCTTAGAGCCAAAATCGGTAGACCTTTAATAATTGCTAAAAATGGCGACATAGCTACCG
 yet Thr Asn His Thr Trp Ala Phe Ser Ile Ala Glu Met Lys Lys Asn Leu Gly Phe Ser His Leu Glu Ile Ile Asn Asp Phe Thr Ala Val Ser Met Ala
 _____gln_____

GAACCCGATGCTGAAAAAGAGCATCTGATTTCAGTTTGGTGGCGCAGAACCGGTGCAAGGTAAAGCCTATTGCGGTTTACGGTGCCGGAACGGGGCTTGGG 2400
 CTTGGGCTACGACTTTTTTCTCGTAGACTAAGTCAAACCCAGCGCTCTTGGCCAGCTTCCATTGCGATAACGCCAAAATGCCACGGCCTTGCCCCGAAACCC
 Asn Pro Met Leu Lys Lys Glu His Leu Ile Gln Phe Gly Ala Glu Pro Val Glu Gly Lys Pro Ile Ala Val Tyr Gly Ala Gly Thr Gly Leu Gly
 _____gln_____

GTTGGCATCTGGTCCATGTCGATAAGCGTTGGTAAGCTTGCCAGGCGAAGGCGGTACGTTGATTTTGGCGCCGAATAGTGAAGAAGAGGCCATTATCC 2500
 CAACGCGTAGACCAGGTACAGCTATTCCGAACCCATTTCGAACGGTCCGCTTCCGCCAGTGCAACTAAACGCGGCTTATCATTCTCTCCGGTAAATAGG
 Val Ala His Leu Val His Val Asp Lys Arg Trp Val Ser Leu Pro Gly Glu Gly His Val Asp Phe Ala Pro Asn Ser Glu Glu Ala Ile Ile
 _____gln_____

TCGAAATATTGGGTGCGGAAATTTGGTTCATGTTTCGGCGGAGGCGTGCCCTTTCTGGCCCTGGGCTGGTGAATTTGTATCGCGCAATTGTGAAAGCTGACAA 2600
 AGCTTTATAACGCACGCCCTTTAACCCAGTACAAAGCCGCTCCGCCACGGAAGACCGGACCCGACCACCTTAAACATAGCGGTTAACACTTTTCGACTGTT
 Leu Glu Ile Leu Arg Ala Glu Ile Gly His Val Ser Ala Glu Ala Cys Leu Ser Gly Pro Gly Leu Val Asn Leu Tyr Arg Ala Ile Val Lys Ala Asp Asn
 _____gln_____

CCGCCTGCCAGAAAAATCTCAAGCCAAAAGATATTACCGAACGCGCGCTGGCTGACAGCTGCACCGGATTCGCCGCGCATTTGTGCGTGTGTTTGGGTGCTATT 2700
 GCGGACGGTCTTTTAGAGTTTCGGTTTCTATAATGGCTTGGCGCGGACCGACTGTCGACGTGGCTAACGGGCGCGTAACAGCGACAAACGCGAGTAA
 Arg Leu Pro Glu Asn Leu Lys Pro Lys Asp Ile Thr Glu Arg Ala Leu Ala Asp Ser Cys Thr Asp Cys Arg Ala Leu Ser Leu Phe Cys Val Ile
 _____gln_____

ATGGGCGGTTTTGGGCGCAATCTGGCGCTCAATCTCGGACATTTGGGCGGTGTTTTATTGGGCGGTATCGTGCGCGCTTCCCTTGTAGTTCTTCAAAG 2800
 TACCCGGCAAAACCGCGTTAGACCGCGAGTTAGAGCCCTGTAAACCGCGCACAAATAACGCCGCCCATAGCACGGCGCGGAAGAACTCAAGAAGTTTC
 Met Gly Arg Phe Gly Asn Leu Ala Leu Asn Leu Gly Thr Phe Gly Gly Val Phe Ile Ala Gly Ile Val Pro Arg Phe Leu Glu Phe Phe Lys
 _____gln_____

GCTCCGGTTTTCCGTGCCGCAATTGAAGATAAAGGGCGCTTAAAGAAATATGTCCATGATATTCCGGTGTATCTCATCTGTCCTGACAAATCCGGGCTTCT 2900
 CGAGGCCAAAGGCACGGCGTAAACTTCTATTTCGCCGGAATTTCTTATACAGGTACTATAAGGCCACATAGAGTAGCAGGTACTGTTAGGCCCGGAAGA
 Gly Ser Gly Phe Arg Ala Ala Phe Glu Asp Lys Gly Arg Phe Lys Glu Tyr Val His Asp Ile Pro Val Tyr Leu Ile Val His Asp Asn Pro Gly Leu Leu
 _____gln_____

CCGATCCGCGTGTAAATGCGGTCTGGAATCCAGTGTAGACATTCCTGTAATCCCTTATAGGAGGAAATATAGCCCTCCATTGAGAGGGCTATTAGAAAAATTTAGTATGT

Gly Ser Gly Ala His Leu Arg Gln Thr Leu Gly His Ile Leu •
_____glk_____

GTTTATTCAATTTTCTTTGTGTCCCTCACAAGGTCGAC 3040
CAATAAGTTAAAAAGAAACACAGGGGAGTGTCCAGCTG